Amendments to the Claims:

This listing of the claims will replace all prior listings of the claims in this application.

1.- 20. (Canceled)

21. (Currently amended) A method of activating a cellular ~~activities~~ activity, said method ~~including~~ comprising:

regulating the activation of phosphorylation of a binding motif of a receptor capable of binding a cytoplasmic protein, said binding motif comprising an amino acid sequence wherein at least one amino acid is serine/threonine; ~~according to any one of claims 1 to 11, a functional equivalent or analogue thereof~~ and

subjecting the binding motif to a cytoplasmic protein wherein said cytoplasmic protein ~~is associated with~~ is capable of mediating a cellular ~~activities~~ activity;

wherein the cellular activity is activated by binding of said cytoplasmic protein with said binding motif.

22. (Currently amended) A method of regulating a cellular ~~activities~~ activity, said method ~~including~~ comprising:

regulating the phosphorylation of a binding motif of a receptor capable of binding a cytoplasmic protein, said binding motif comprising an amino acid sequence wherein at least one amino acid is serine/threonine; ~~according to any one of claims 1 to 11-, a functional equivalent or analogue thereof~~

subjecting the binding motif to a cytoplasmic protein to bind the cytoplasmic protein to the binding motif; and

activating a cell signaling pathway by interacting the bound cytoplasmic protein with a signaling molecule involved in the pathway;

wherein the cellular activity is regulated by the activated cell signaling pathway.

23. (Canceled)

24. (Currently amended) A method according to ~~any one of~~ claims 21 ~~to 23~~ or 22, wherein the cellular ~~activities~~ activity ~~or cell signalling pathways~~ ~~are~~ is selected from the group ~~including~~ consisting of cell survival, proliferation, transformation, differentiation, mitogenesis, chemotaxis, motility, enhanced phagocytosis, bacterial killing, superoxide production and cytotoxicity.

25.-29. (Canceled)

30. (New) A method according to claim 21 or 22, wherein the serine/threonine residue corresponds to a serine residue at position 585 of the common βc according to Figure 1 (SEQ ID NO:1).

31. (New) A method according to claim 21 or 22, wherein at least two (2) amino acids are serine.

32. (New) A method according to claim 21 or 22, wherein the amino acid sequence includes the sequence

-S-X-S/T- (SEQ ID NO:2)

wherein the X is any amino acid.

33. (New) A method according to claim 32, further including flanking amino acids selected from R and X-P wherein X is any amino acid such that the flanking amino acids individually or co-operatively contribute to the binding motif for binding to a cytoplasmic protein.

34. (New) A method according claim 21 or 22, wherein the amino acid sequence of the binding motif includes the sequence:

-R-S-X-S/T-X-P- (SEQ ID NO:3)

wherein X is any amino acid.

35. (New) A method according to claim 21 or 22, wherein the receptor is the GM-CSF/IL-3/IL-5 receptor.

36. (New) A method according to claim 21 or 22, wherein the amino acid sequence is HSRSLP (SEQ ID NO:4).

37. (New) A method according to claim 21 or 22, wherein the receptor is the GM-CSF/IL-3/IL-5 receptor and comprises a sequence which includes amino acids HSRSLP (SEQ ID NO:4) corresponding to amino acids 582 to 587 of the common βc according to Figure 1 (SEQ ID NO:1).

38. (New) A method according to claim 21 or 22, wherein the motif corresponds to any one of the following:

Stem Cell Growth Factor Receptor (C-Kit) (Proto-Oncogene Tyrosine- Protein Kinase Kit) (C-KIT) (CD 117 Antigen), including amino acids 863 to 869 according to Figure 2 (SEQ ID NO:32) or amino acid residues 965 to 969 according to Figure 2 (SEQ ID NO:32);

Thrombopoietin Receptor Precursor (TPO-R) (Myeloproliferative Leukemia Protein) (C-MPL), (TPOR or MPL) including amino acids 573 to 579 according to Figure 3 (SEQ ID NO:33);

Thrombopoietin Receptor Precursor (TPO-R) (Myeloproliferative Leukemia Protein) (C-MPL), (TPOR or MPL) including amino acids 564 to 570 according to Figure 4 SEQ ID NO:34);

IL6B HUMAN interleukin-6 receptor beta chain precursor (IL-6R-BETA), including amino acids 735- 739 having the sequence SSSRP (SEQ ID NO:5);

LEPR HUMAN leptin receptor precursor (LEP-R) (OB receptor) (OB-R), including amino acids

991- 995 having the sequence SNSKP (SEQ ID NO:6);

TNR2 HUMAN tumor necrosis factor receptor 2 precursor (tumor necrosis factor) including amino acids 368- 372 having the sequence SDSSP (SEQ ID NO:7);

VGR1 HUMAN vascular endothelial growth factor receptor 1 precursor, including amino acids 1197- 1201 having the sequence SISAP (SEQ ID NO:8);

TRK3 HUMAN receptor protein-tyrosine kinase TKT precursor (EC 2.7.1.112), including amino acids 444- 448, having the sequence SLSLP (SEQ ID NO:9);

Q01974 protein-tyrosine kinase transmembrane receptor ROR2 precursor, including amino acids 435- 439, having the sequence SASTP (SEQ ID NO:10);

FGR1 HUMAN basic fibroblast growth factor receptor 1 precursor (BFGF-R), including amino acids 777- 781, having the sequence SPSFP (SEQ ID NO:11);

Q15426 protein-tyrosine phosphatase, receptor-type, H precursor (EC 3.1.3.48), including amino acids 1082- 1086, having the sequence SNSQP (SEQ ID NO:12);

PTPM HUMAN protein-tyrosine phosphatase MU precursor (EC 3.1.3.48) (R-PTP-MU), including amino acids 818- 822, 833- 837, 1082- 1086 having the sequences SVSSP (SEQ ID NO:13), STSVP (SEQ ID NO:14), SKSPP (SEQ ID NO:15);

PGDS HUMAN alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112), including amino acids 616- 620 having the sequence SRSQP (SEQ ID NO:16);

FGR4 HUMAN fibroblast growth factor receptor 4 precursor (FGFR-4) (EC 2.7.1.112), including amino acids 439- 443, 791- 795 having the sequences SSSGP (SEQ ID NO:18), SSSFP (SEQ ID

NO:19);

FGR2 HUMAN fibroblast growth factor receptor 2 precursor (FGFR-2) (EC 2.7.1.112), including amino acids 780- 784 having the sequence SPSYP (SEQ ID NO:20);

Q13635 patched protein homolog (PTC), including amino acids 1290- 1294 having the sequence SGSLP (SEQ ID NO:21);

MAN4R HUMAN macrophage mannose receptor precursor, including amino acids 1432-1436 having the sequence SQSSP (SEQ ID NO:22);

LRP2 HUMAN low-density lipoprotein receptor-related protein 2 precursor (megalin), including amino acids 4616- 4620 having the sequence SPSLP (SEQ ID NO:23);

IDD HUMAN integral membrane protein DGCR2/IDD precursor (KTAAO163), including amino acids 526- 530 having the sequence SGSTP (SEQ ID NO:24);

AMFR HUMAN autocrine motility factor receptor precursor (AMF receptor) (GP78), including amino acids 203- 207 having the sequence SVSPP (SEQ ID NO:25); and

ACH5 HUMAN neuronal acetylcholine receptor protein, alpha-S chain precursor, including amino acids 382-386 having the sequence SGSGP (SEQ ID NO:26).

39. (New) A method according to claim 21 or 22, wherein at least one serine residue of the amino acid sequence is phosphorylated.

40. (New) A method according to claim 39, wherein a second serine residue from the 5' end of the motif is phosphorylated.

41. (New) A method according to claim 39, wherein the serine residue is at position 585 of the common βc according to Figure 1 (SEQ ID NO:1).

42. (New) A method according to claim 39, wherein the receptor is a GM-CSF/IL-3/IL-5 receptor capable of binding a cytoplasmic protein, said binding motif comprising an amino acid sequence including the sequence ^{582}HSRSLP^{587} (SEQ ID NO:4) of the GM-CSF/IL-3/IL-5 receptor or a functional equivalent or analogue thereof wherein at least Ser^{585} is capable of being phosphorylated.

43. (New) A method of activating cell survival in a cell said method comprising:

introducing a change in phosphorylation of a binding motif of a receptor that is capable of binding a cytoplasmic protein, said binding motif comprising an amino acid sequence comprising the sequence –S–X–S/T– wherein X is any amino acid; and

subjecting the binding motif to a cytoplasmic protein wherein said cytoplasmic protein is capable of mediating cell survival;

wherein the cell survival is activated by binding of said cytoplasmic protein with said binding motif.

44. (New) A method of regulating cell survival in a cell, said method comprising:

introducing a change in phosphorylation of a binding motif of a receptor that is capable of binding a cytoplasmic protein, said binding motif comprising an amino acid sequence comprising the sequence –S–X–S/T– wherein X is any amino acid; and

subjecting the binding motif to a cytoplasmic protein to bind the cytoplasmic protein to the binding motif; and

activating a cell signaling pathway by interacting the bound cytoplasmic protein with a signaling molecule involved in the pathway;

wherein the cell survival is regulated by the activated cell signaling pathway.

45. (New) A method according to claim 44, wherein the serine/threonine residue corresponds to a serine residue at position 585 of the common βc according to Figure 1 (SEQ ID NO:l).

46. (New) A method according to claim 44, further including flanking amino acids selected from R and X-P wherein X is any amino acid such that the flanking amino acids individually or co-operatively contribute to the binding motif for binding to a cytoplasmic protein.

47. (New) A method according claim 43 or 44, wherein the amino acid sequence of the binding motif includes the sequence:

-R-S-X-S/T-X-P- (SEQ ID NO:3)

wherein X is any amino acid.

48. (New) A method according to claim 43 or 44, wherein the receptor is the GM-CSF/IL-3/IL-5 receptor.

49. (New) A method according to claim 43 or 44, wherein the amino acid sequence is HSRSLP (SEQ ID NO:4).

50. (New) A method according to claim 43 or 44, wherein the receptor is the GM-CSF/IL-3/IL-5 receptor and comprises a sequence which includes amino acids HSRSLP (SEQ ID NO:4) corresponding to amino acids 582 to 587 of the common βc according to Figure 1 (SEQ ID NO:1).

51. (New) A method according to claim 43 or 44, wherein the motif corresponds to any one of the following:

Stem Cell Growth Factor Receptor (C-Kit) (Proto-Oncogene Tyrosine- Protein Kinase Kit) (C-KIT) (CD 117 Antigen), including amino acids 863 to 869 according to Figure 2 (SEQ ID NO:32) or amino acid residues 965 to 969 according to Figure 2 (SEQ ID NO:32);

Thrombopoietin Receptor Precursor (TPO-R) (Myeloproliferative Leukemia Protein) (C-MPL),

(TPOR or MPL) including amino acids 573 to 579 according to Figure 3 (SEQ ID NO:33);

Thrombopoietin Receptor Precursor (TPO-R) (Myeloproliferative Leukemia Protein) (C-MPL), (TPOR or MPL) including amino acids 564 to 570 according to Figure 4 SEQ ID NO:34);

IL6B HUMAN interleukin-6 receptor beta chain precursor (IL-6R-BETA), including amino acids 735- 739 having the sequence SSSRP (SEQ ID NO:5);

LEPR HUMAN leptin receptor precursor (LEP-R) (OB receptor) (OB-R), including amino acids 991- 995 having the sequence SNSKP (SEQ ID NO:6);

TNR2 HUMAN tumor necrosis factor receptor 2 precursor (tumor necrosis factor) including amino acids 368- 372 having the sequence SDSSP (SEQ ID NO:7);

VGR1 HUMAN vascular endothelial growth factor receptor 1 precursor, including amino acids 1197- 1201 having the sequence SISAP (SEQ ID NO:8);

TRK3 HUMAN receptor protein-tyrosine kinase TKT precursor (EC 2.7.1.112), including amino acids 444- 448, having the sequence SLSLP (SEQ ID NO:9);

Q01974 protein-tyrosine kinase transmembrane receptor ROR2 precursor, including amino acids 435- 439, having the sequence SASTP (SEQ ID NO:10);

FGR1 HUMAN basic fibroblast growth factor receptor 1 precursor (BFGF-R), including amino acids 777- 781, having the sequence SPSFP (SEQ ID NO:11);

Q15426 protein-tyrosine phosphatase, receptor-type, H precursor (EC 3.1.3.48), including amino acids 1082- 1086, having the sequence SNSQP (SEQ ID NO:12);

PTPM HUMAN protein-tyrosine phosphatase MU precursor (EC 3.1.3.48) (R-PTP-MU), including amino acids 818- 822, 833- 837, 1082- 1086 having the sequences SVSSP (SEQ ID NO:13), STSVP (SEQ ID NO:14), SKSPP (SEQ ID NO:15);

PGDS HUMAN alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112), including amino acids 616- 620 having the sequence SRSQP (SEQ ID NO:16);

FGR4 HUMAN fibroblast growth factor receptor 4 precursor (FGFR-4) (EC 2.7.1.112), including amino acids 439- 443, 791- 795 having the sequences SSSGP (SEQ ID NO:18), SSSFP (SEQ ID NO:19);

FGR2 HUMAN fibroblast growth factor receptor 2 precursor (FGFR-2) (EC 2.7.1.112), including amino acids 780- 784 having the sequence SPSYP (SEQ ID NO:20);

Q13635 patched protein homolog (PTC), including amino acids 1290- 1294 having the sequence SGSLP (SEQ ID NO:21);

MAN4R HUMAN macrophage mannose receptor precursor, including amino acids 1432-1436 having the sequence SQSSP (SEQ ID NO:22);

LRP2 HUMAN low-density lipoprotein receptor-related protein 2 precursor (megalin), including amino acids 4616- 4620 having the sequence SPSLP (SEQ ID NO:23);

IDD HUMAN integral membrane protein DGCR2/IDD precursor (KTAAO163), including amino acids 526- 530 having the sequence SGSTP (SEQ ID NO:24);

AMFR HUMAN autocrine motility factor receptor precursor (AMF receptor) (GP78), including amino acids 203- 207 having the sequence SVSPP (SEQ ID NO:25); and

ACH5 HUMAN neuronal acetylcholine receptor protein, alpha-S chain precursor, including amino acids 382-386 having the sequence SGSGP (SEQ ID NO:26).

52. (New) A method according to claim 43 or 44, wherein at least one serine residue of the amino acid sequence is phosphorylated.

53. (New) A method according to claim 52, wherein a second serine residue from the 5' end of the motif is phosphorylated.

54. (New) A method according to claim 52, wherein the receptor is a GM-CSF/IL-3/IL-5 receptor capable of binding a cytoplasmic protein, said binding motif comprising an amino acid sequence including the sequence ^{582}HSRSLP^{587} (SEQ ID NO:4) of the GM-CSF/IL-3/IL-5 receptor wherein at least Ser^{585} is capable of being phosphorylated.

55. (New) A method according to claim 43 or 44, wherein the change is introduced by a mutation of the binding motif.

56. (New) A method according to claim 55, wherein the mutation is at position 585 of the common βc according to Figure 1 (SEQ ID NO:l).

57. (New) A method according to claim 43 or 44, wherein the change is introduced by exposing the binding motif to an agonist or antagonist of the binding motif.

58. (New) A method according to claim 57, wherein the agonist or antagonist is directed to a serine at position 585 of the common βc according to Figure 1 (SEQ ID NO:l).

59. (New) A method of inhibiting cell survival in a cell, said method comprising:

introducing a change in phosphorylation that inhibits phosphorylation of a binding motif of βc of a receptor that is capable of binding a cytoplasmic protein, said binding motif comprising an

amino acid sequence comprising the sequence –S-X-S/T-, wherein X is any amino acid.

60. (New) A method according to claim 59, wherein the serine/threonine residue corresponds to a serine residue at position 585 of the common βc according to Figure 1 (SEQ ID NO:1).

61. (New) A method according to claim 59, further including flanking amino acids selected from R and X-P wherein X is any amino acid such that the flanking amino acids individually or co-operatively contribute to the binding motif for binding to a cytoplasmic protein.

62. (New) A method according claim 59, wherein the amino acid sequence of the binding motif includes the sequence:

-R-S-X-S/T-X-P- (SEQ ID NO:3)

wherein X is any amino acid.

63. (New) A method according to claim 59, wherein the receptor is the GM-CSF/IL-3/IL-5 receptor.

64. (New) A method according to claim 59, wherein the amino acid sequence is HSRSLP (SEQ ID NO:4).

65. (New) A method according to claim 59, wherein the receptor is the GM-CSF/IL-3/IL-5 receptor and comprises a sequence which includes amino acids HSRSLP (SEQ ID NO:4) corresponding to amino acids 582 to 587 of the common βc according to Figure 1 (SEQ ID NO:1).

66. (New) A method according to claim 59, wherein the change is introduced by a mutation of the binding motif.

67. (New) A method according to claim 63, wherein the mutation is at position 585 of the common βc according to Figure 1 (SEQ ID NO:1).

68. (New) A method according to claim 59, wherein the change is introduced by exposing the binding motif to an agonist or antagonist of the binding motif.

69. (New) A method according to claim 68, wherein the agonist or antagonist is directed to a serine at position 585 of the common βc according to Figure 1 (SEQ ID NO:l).

70. (New) A method according to claim 59, wherein the cell is a haematopoietic cell.

71. (New) A method according to claim 70, wherein the haematopoietic cell is a leukocyte.

72. (New) A method according to claim 22, wherein the cell signaling pathway is selected from the group consisting of cell survival, proliferation, transformation, differentiation, mitogenesis, chemotaxis, motility, enhanced phagocytosis, bacterial killing, superoxide production and cytotoxicity.